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Sequence Listing could not be accepted.

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217-9197 (toll free).

Reviewer: markspencer

Timestamp: Thu May 24 14:13:01 EDT 2007

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Reviewer Comments:

<210> 1

<211> 1629

<212> DNA

<213> Unknown

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The use of "Environmental", for numeric identifier <223>, is
insufficient. Please
explain the source of the genetic material. When Unknown is used for the
organism.

The source can be a broad category such as Mammalian, Bacterial,
Viral...etc.

Note, several sequences need this change.

Application No: 10576122 Version No: 1.0

Input Set:

Output Set:

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Finished: 2007-05-23 23:04:23.508
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 413 ms
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Total Errors: 0
No. of SeqIDs Defined: 6
Actual SeqID Count: 6

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)

SEQUENCE LISTING

<110> MORGAN, Brian
 BURK, Mark
 LEVIN, Michael
 ZHU, Zoulin
 CHAPLIN, Jennifer
 KUSTEDJO, Karen
 HUANG, Zilin
 GREENBERG, William

<120> METHODS FOR MAKING SIMVASTATIN AND INTERMEDIATES

<130> 564462012800

<140> 10576122

<141> 2007-05-23

<150> US 10/576,122

<151> 2004-10-20

<150> PCT/US2004/034913

<151> 2004-10-20

<150> US 60/542,100

<151> 2004-02-04

<150> US 60/513,237

<151> 2003-10-21

<160> 6

<170> PatentIn version 3.1

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<211> 542

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<213> Unkown

<220>

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<222> (1)...(24)

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Gly Leu Glu Leu Pro Tyr Thr Thr Ile Thr Ser Ala Ala Val Ala Thr	35	40	45
Glu Gly Pro Ile Pro Gln Pro Ala Ile Phe Gly Ser Thr Asp Pro Ile	50	55	60
Val Ala Pro Glu Arg Cys Glu Val Arg Ala Val Thr Arg Pro Thr Lys	65	70	75
Asp Ser Glu Ile Arg Ile Glu Leu Trp Leu Pro Leu Ser Gly Trp Asn	85	90	95
Gly Lys Tyr Leu Gln Ile Gly Ser Gly Gly Trp Ala Gly Ser Ile Asn	100	105	110
Arg Thr Gly Leu Ile Gly Pro Leu Gln Arg Gly Tyr Ala Val Ala Ala	115	120	125
Thr Asp Asn Gly His Ile Ser Glu Gly Leu Val Pro Asp Ala Ser Trp	130	135	140
Ala Ile Gly His Pro Gln Lys Leu Ile Asp Phe Gly Tyr Arg Ala Val	145	150	155
His Glu Thr Ser Val Gln Ala Lys Ala Ile Leu Arg Ala Tyr Phe Gly	165	170	175
Arg Gly Gln Asp Leu Ser Tyr Phe Ser Gly Cys Ser Asn Gly Gly Arg	180	185	190
Glu Ala Leu Met Glu Ala Gln Arg Tyr Pro Glu Asp Phe Glu Gly Ile	195	200	205
Ile Ala Gly Ala Pro Ala Asn Asn Trp Ser Arg Leu Phe Thr Gly Phe	210	215	220
Val Trp Asn Glu Arg Ala Leu Ala Asp Asp Pro Ile Pro Pro Ala Lys	225	230	235
			240

Leu Thr Ala Ile Gln Ala Ala Ala Ile Ala Ala Cys Asp Thr Leu Asp
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Gly Val Glu Asp Gly Leu Ile Glu Asn Pro Arg Ala Cys Ser Phe Asp
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Pro Arg Ser Met Val Cys Thr Ala Asp Asp Ala Ser Asp Cys Leu Thr
275 280 285

Glu Gly Gln Val Ala Thr Leu His Arg Ile Tyr Ser Gly Pro Thr Asn
290 295 300

Pro Arg Thr Gly Glu Arg Ile Phe Pro Gly Tyr Pro Met Gly Thr Glu
305 310 315 320

Ala Val Pro Gly Gly Trp Val Pro Trp Ile Val Ser Ala Ser Ser Glu
325 330 335

Val Pro Ser Ile Gln Ala Ser Phe Gly Asn Ser Tyr Tyr Gly His Ala
340 345 350

Val Phe Glu Gln Ser Asn Trp Asp Phe Arg Thr Leu Asp Phe Asp Gln
355 360 365

Asp Val Ala Phe Gly Asp Ala Lys Ala Gly Pro Val Leu Asn Ala Thr
370 375 380

Asn Pro Asp Leu Arg Ser Phe Arg Ala Asn Gly Gly Lys Leu Ile Gln
385 390 395 400

Tyr His Gly Trp Gly Asp Ala Ala Ile Thr Ala Phe Ser Ser Ile Asp
405 410 415

Tyr Tyr Glu Asn Val Arg Ala Phe Leu Asp Arg Phe Pro Asp Pro Arg
420 425 430

Ser Glu Asn Thr Asp Ile Asp Gly Phe Tyr Arg Leu Phe Leu Val Pro
435 440 445

Gly Met Gly His Cys Ser Gly Gly Ile Gly Pro Ser Ser Phe Gly Asn
450 455 460

Gly Phe Arg Ser Ala Arg Thr Asp Ala Glu His Asp Leu Leu Ser Ala
465 470 475 480

Leu Glu Ala Trp Val Glu Arg Asp Thr Ala Pro Glu Arg Leu Ile Gly
485 490 495

Thr Gly Thr Ala Val Gly Asp Pro Thr Ala Thr Leu Thr Arg Pro Leu
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<210> 3

<211> 1209

<212> DNA

<213> Unknown

<220>

<223> Environmental

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gtagtggaact tgtggggcgg catggcgct gccgacactc agacgccatg gacggcggag 180

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ttccaagagg agatcgccag gccgttgggg ttagatttct ggattggctt accagcagag 600

caagaggcac gggtcgcgcc gatgatcgcg gcggagcctg atccgcaaag cctcttcttc 660

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<212> PRT

<213> Unkown

<220>

<223> Environmental

<220>

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<222> (18)...(386)

<223> Beta-lactamase

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          20           25           30

```

```

Cys Val Thr Leu His Gly Glu Thr Val Val Asp Leu Trp Gly Gly Met
          35           40           45

```

```

Ala Arg Ala Asp Thr Gln Thr Pro Trp Thr Ala Glu Thr Val Ser Ile
          50           55           60

```

```

Val Phe Ser Ser Thr Lys Gly Ala Thr Ala Leu Cys Ala His Met Leu
        65           70           75           80

```

```

Ala Ser Arg Gly Gln Leu Asp Leu Asp Ala Pro Val Ala Thr Tyr Trp
          85           90           95

```

```

Pro Glu Phe Ala Gln Ala Gly Lys Ala Arg Ile Pro Val Lys Met Leu
          100          105          110

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Leu	Asn	His	Gln	Ala	Gly	Leu	Pro	Ala	Val	Arg	Thr	Pro	Leu	Pro	Gln	115	120	125
Gly	Ala	Tyr	Ala	Asp	Trp	Glu	Leu	Met	Val	Asn	Thr	Leu	Ala	Lys	Glu	130	135	140
Glu	Pro	Phe	Trp	Glu	Pro	Gly	Thr	Arg	Asn	Gly	Tyr	His	Ala	Leu	Thr	145	150	155
Met	Gly	Trp	Leu	Val	Gly	Glu	Val	Val	Arg	Arg	Val	Ser	Gly	Lys	Ser	165	170	175
Leu	Gly	Thr	Phe	Phe	Gln	Glu	Glu	Ile	Ala	Arg	Pro	Leu	Gly	Leu	Asp	180	185	190
Phe	Trp	Ile	Gly	Leu	Pro	Ala	Glu	Gln	Glu	Ala	Arg	Val	Ala	Pro	Met	195	200	205
Ile	Ala	Ala	Glu	Pro	Asp	Pro	Gln	Ser	Leu	Phe	Phe	Gln	Glu	Val	Ala	210	215	220
Lys	Pro	Gly	Ala	Leu	Gln	Ser	Leu	Val	Leu	Leu	Asn	Ser	Gly	Gly	Tyr	225	230	235
Met	Gly	Ala	Gln	Pro	Glu	Tyr	Asp	Ser	Arg	Ala	Ala	His	Ala	Ala	Glu	245	250	255
Ile	Gly	Ala	Ala	Gly	Gly	Ile	Thr	Asn	Ala	Arg	Gly	Leu	Ala	Gly	Met	260	265	270
Tyr	Ala	Pro	Leu	Ala	Cys	Gly	Gly	Lys	Leu	Lys	Gly	Val	Glu	Leu	Val	275	280	285
Ser	Pro	Asp	Met	Leu	Ala	Arg	Met	Ser	Arg	Val	Ala	Ser	Ala	Thr	Gly	290	295	300
Arg	Asp	Ala	Val	Leu	Met	Met	Pro	Thr	Arg	Phe	Ala	Leu	Gly	Phe	Met	305	310	315
Lys	Ser	Met	Asp	Asn	Arg	Arg	Glu	Pro	Ala	Gly	Val	Gln	Asp	Ser	Ala	325	330	335

Leu Phe Gly Glu Glu Ala Phe Gly His Val Gly Ala Gly Gly Ser Phe
340 345 350

Gly Phe Ala Asp Pro Lys Ala Gly Met Ser Phe Gly Tyr Thr Met Asn
355 360 365

Arg Met Gly Leu Gly Ala Gly Leu Asn Pro Arg Gly Gln Ser Leu Val
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Asp Ala Thr Tyr Arg Ser Leu Gly Tyr Gln Ser Asp Ala Ser Gly Ala
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<211> 1578

<212> DNA

<213> Unknown

<220>

<223> Environmental

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ccgccggaac actcctatct catcgggtgc tcatcgggtg ggtaccaggg cctgatggag 600

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<210> 6

<211> 525

<212> PRT

<213> Unkown

<220>

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<222> (1)...(25)

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          20           25           30

```

```

Cys Ala Asp Leu Ala Asn Gln Gln Leu Pro Asn Thr Thr Ile Thr Ser
          35           40           45

```

```

Ala Gln Thr Val Thr Thr Gly Ser Leu Thr Pro Pro Gly Ser Thr Asn
          50           55           60

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```

Pro Ile Thr Asp Leu Pro Pro Phe Cys Arg Val Thr Gly Ala Ile Ala

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	100		105		110	
Ile Ile Ser Phe Gly Ala Leu Gly Ser Gln Leu Lys Arg Gly Tyr Ala						
	115		120		125	
Thr Ala Ser Thr Asn Thr Gly His Glu Ala Ala Pro Gly Met Asn Ala						
	130		135		140	
Ala Arg Phe Ala Phe Glu Lys Pro Glu Gln Leu Ile Asp Phe Ala Tyr						
	145		150		155	160
Arg Ser Gln His Glu Thr Ala Leu Lys Ala Lys Ala Leu Val Gln Ala						
	165		170		175	
Phe Tyr Gly Lys Pro Pro Glu His Ser Tyr Phe Ile Gly Cys Ser Ser						
	180		185		190	
Gly Gly Tyr Gln Gly Leu Met Glu Ala Gln Arg Phe Pro Ala Asp Tyr						
	195		200		205	
Asp Gly Ile Val Ala Gly Met Pro Ala Asn Asn Trp Thr Arg Leu Met						
	210		215		220	
Ala Gly Asp Leu Asp Ala Ile Leu Ala Val Ser Val Asp Pro Ala Ser						
	225		230		235	240
His Leu Pro Val Ser Ala Leu Gly Leu Leu Tyr Arg Ser Val Leu Ala						
	245		250		255	
Ala Cys Asp Gly Ile Asp Gly Val Val Asp Gly Val Leu Glu Asp Pro						
	260		265		270	
Arg Arg Cys Arg Phe Asp Pro Ala Val Leu Met Cys Lys Ala Asp Gln						
	275		280		285	
Asn Pro Asp Gly Cys Leu Thr Pro Ala Gln Val Glu Ala Ala Arg Arg						
	290		295		300	

Ile Tyr Gly Gly Leu Lys Asp Pro Lys Thr Gly Ala Gln Leu Tyr Pro
305 310 315 320

Gly Leu Ala Pro Gly Ser Glu Pro Phe Trp Pro His Arg Asn Pro Ala
325 330 335

Asn Pro Phe Pro Ile Pro Ile Ala His Tyr Lys Trp Leu Val Phe Ala
340 345 350

Asp Pr